

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/502,510B
Source: IFWP
Date Processed by STIC: 8/14/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/502,870B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 08/14/2006

PATENT APPLICATION: US/10/502,510B

TIME: 12:24:23

Input Set : E:\04-585SeqListingST25.TXT

Output Set: N:\CRF4\08142006\J502510B.raw

3 <110> APPLICANT: El-Gewely, Mohamed Raafat
 4 El-Gewely, Mohamed Raafat
 5 Gardner, Rebecca
 7 <120> TITLE OF INVENTION: Methods of screening molecular libraries and active
 molecules
 8 identified thereby
 10 <130> FILE REFERENCE: MBHB-04-585 (59.68.75763/001)
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/502,510B
 C--> 12 <141> CURRENT FILING DATE: 2004-07-23
 12 <150> PRIOR APPLICATION NUMBER: PCT/GB03/00291
 13 <151> PRIOR FILING DATE: 2003-01-03
 15 <160> NUMBER OF SEQ ID NOS: 51
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 21
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: secretion signal peptide
 28 <220> FEATURE:
 29 <221> NAME/KEY: UNSURE
 30 <222> LOCATION: (1)..(21)
 31 <223> OTHER INFORMATION: secretion signal peptide
 33 <400> SEQUENCE: 1
 35 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 36 1 5 10 15
 39 Gly Ser Thr Gly Asp
 40 20
 43 <210> SEQ ID NO: 2
 44 <211> LENGTH: 49
 45 <212> TYPE: PRT
 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: transmembrane domain
 52 <220> FEATURE:
 53 <221> NAME/KEY: UNSURE
 54 <222> LOCATION: (1)..(49)
 55 <223> OTHER INFORMATION: transmembrane domain
 57 <400> SEQUENCE: 2
 59 Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
 60 1 5 10 15
 63 Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
 64 20 25 30
 67 Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro

see pp 2, 4, 6
 Does Not Comply
 Corrected Diskette Needed

DATE: 08/14/2006

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Output Set: N:\CRF4\08142006\J502510B.raw

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35              40              45
71 Arg
75 <210> SEQ ID NO: 3
76 <211> LENGTH: 5
77 <212> TYPE: PRT
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: peptide derivative
84 <220> FEATURE:
85 <221> NAME/KEY: VARIANT
86 <222> LOCATION: (1)..(5)
87 <223> OTHER INFORMATION: peptide derivative
89 <400> SEQUENCE: 3
91 Met Gly Trp Cys Thr
92 1 5
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 190
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
100 <220> FEATURE:
101 <223> OTHER INFORMATION: vector
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (1)..(190)
107 <223> OTHER INFORMATION: vector
109 <220> FEATURE:
110 <221> NAME/KEY: variation
111 <222> LOCATION: (1)..(190)
112 <223> OTHER INFORMATION: n= A, C, G or T in equal molar ratio
114 <220> FEATURE:
115 <221> NAME/KEY: variation
116 <222> LOCATION: (1)..(190)
117 <223> OTHER INFORMATION: k= G or T in equal molar ratio
119 <400> SEQUENCE: 4
120 ttgacgcaaa tgggcggtag gcggtgacgg tgggaggtct atataagcag agctcggtta
122 gtgaaccgctc agatctctag aagctgggta ccagctgcta gcaagcttgc tagcggccgc
124 tcgaggccgg caaggccgga tccagacatg ataagatata ttgatgagtt tggacaaacc
126 acaactagaa
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 70
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: vector
138 <220> FEATURE:
139 <221> NAME/KEY: misc_feature
140 <222> LOCATION: (1)..(70)
141 <223> OTHER INFORMATION: vector
143 <220> FEATURE:

```

no n's in this
sequence.

no k's in this sequence

RAW SEQUENCE LISTING DATE: 08/14/2006
 PATENT APPLICATION: US/10/502,510B TIME: 12:24:23
 Input Set : E:\04-585SeqListingST25.TXT
 Output Set: N:\CRF4\08142006\J502510B.raw

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144 <221> NAME/KEY: variation
145 <222> LOCATION: (1)..(70)
146 <223> OTHER INFORMATION: n= A, C, G or T in equal molar ratio
148 <220> FEATURE:
149 <221> NAME/KEY: variation
150 <222> LOCATION: (1)..(70)
151 <223> OTHER INFORMATION: k= G or T in equal molar ratio
153 <400> SEQUENCE: 5
W--> 154 aagagctcgg taccaagaag gagtttacat atgggannkn nknnktgata aggatccaag 60
156 cttgaattca 70
159 <210> SEQ ID NO: 6
160 <211> LENGTH: 23
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: synthetic sequence
168 <220> FEATURE:
169 <221> NAME/KEY: misc_feature
170 <222> LOCATION: (1)..(23)
171 <223> OTHER INFORMATION: synthetic sequence
173 <400> SEQUENCE: 6
174 aagagctcgg taccaagaag gag 23
177 <210> SEQ ID NO: 7
178 <211> LENGTH: 25
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: synthetic sequence
186 <220> FEATURE:
187 <221> NAME/KEY: misc_feature
188 <222> LOCATION: (1)..(25)
189 <223> OTHER INFORMATION: synthetic sequence
191 <400> SEQUENCE: 7
192 ctgaattcaa gcttgatcc ttatc 25
195 <210> SEQ ID NO: 8
196 <211> LENGTH: 20
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: primer
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (1)..(20)
207 <223> OTHER INFORMATION: primer
209 <400> SEQUENCE: 8
210 agagctcggt tagtgaaccg 20
213 <210> SEQ ID NO: 9
214 <211> LENGTH: 20
215 <212> TYPE: DNA

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/502,510B

DATE: 08/14/2006

TIME: 12:24:23

Input Set : E:\04-585SeqListingST25.TXT

Output Set: N:\CRF4\08142006\J502510B.raw

216 <213> ORGANISM: Artificial Sequence
 218 <220> FEATURE:
 219 <223> OTHER INFORMATION: primer
 222 <220> FEATURE:
 223 <221> NAME/KEY: misc_feature
 224 <222> LOCATION: (1)..(20)
 225 <223> OTHER INFORMATION: primer
 227 <400> SEQUENCE: 9
 228 gtggtttgtc caaactcatc
 231 <210> SEQ ID NO: 10
 232 <211> LENGTH: 55
 233 <212> TYPE: DNA
 234 <213> ORGANISM: Artificial Sequence
 236 <220> FEATURE:
 237 <223> OTHER INFORMATION: library sequence
 240 <220> FEATURE:
 241 <221> NAME/KEY: misc_feature
 242 <222> LOCATION: (1)..(55)
 243 <223> OTHER INFORMATION: library sequence
 245 <400> SEQUENCE: 10
 246 ggtaccaaga aggagtttac atatgggatg gtgtacttga taaggatcca agctt
 249 <210> SEQ ID NO: 11
 250 <211> LENGTH: 20
 251 <212> TYPE: DNA
 252 <213> ORGANISM: Artificial Sequence
 254 <220> FEATURE:
 255 <223> OTHER INFORMATION: primer
 258 <220> FEATURE:
 259 <221> NAME/KEY: misc_feature
 260 <222> LOCATION: (1)..(20)
 261 <223> OTHER INFORMATION: primer
 263 <400> SEQUENCE: 11
 264 ctacctcagg cagctcaagc
 267 <210> SEQ ID NO: 12
 268 <211> LENGTH: 20
 269 <212> TYPE: DNA
 270 <213> ORGANISM: Artificial Sequence
 272 <220> FEATURE:
 273 <223> OTHER INFORMATION: primer
 276 <220> FEATURE:
 277 <221> NAME/KEY: misc_feature
 278 <222> LOCATION: (1)..(20)
 279 <223> OTHER INFORMATION: primer
 281 <400> SEQUENCE: 12
 282 agacagcacc ctcacatgc
 285 <210> SEQ ID NO: 13
 286 <211> LENGTH: 20
 287 <212> TYPE: DNA
 288 <213> ORGANISM: Artificial Sequence

20

55

20

20

*insufficient
 explanation - what is
 the source of
 the genetic material?
 (see
 item 11
 on Erra
 summary
 sheet)*

*Please
 correct these
 types of
 errors in
 subsequent
 sequences*

RAW SEQUENCE LISTING

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PATENT APPLICATION: US/10/502,510B

TIME: 12:24:23

Input Set : E:\04-585SeqListingST25.TXT

Output Set: N:\CRF4\08142006\J502510B.raw

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290 <220> FEATURE:
291 <223> OTHER INFORMATION: primer
294 <220> FEATURE:
295 <221> NAME/KEY: misc_feature
296 <222> LOCATION: (1)..(20)
297 <223> OTHER INFORMATION: primer
299 <400> SEQUENCE: 13
300 tgggtgctcat cttaatggcc 20
303 <210> SEQ ID NO: 14
304 <211> LENGTH: 20
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: primer
312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: (1)..(20)
315 <223> OTHER INFORMATION: primer
317 <400> SEQUENCE: 14
318 tgacaaaacc taacttgccg 20
321 <210> SEQ ID NO: 15
322 <211> LENGTH: 26
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: primer
330 <220> FEATURE:
331 <221> NAME/KEY: misc_feature
332 <222> LOCATION: (1)..(26)
333 <223> OTHER INFORMATION: primer
335 <400> SEQUENCE: 15
336 aagcagtggg aacaacgcag agtact 26
339 <210> SEQ ID NO: 16
340 <211> LENGTH: 23
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: primer
348 <220> FEATURE:
349 <221> NAME/KEY: misc_feature
350 <222> LOCATION: (1)..(23)
351 <223> OTHER INFORMATION: primer
353 <400> SEQUENCE: 16
354 aagcagtggg aacaacgcag agt 23
357 <210> SEQ ID NO: 17
358 <211> LENGTH: 34
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/14/2006
PATENT APPLICATION: US/10/502,510B TIME: 12:24:25

Input Set : E:\04-585SeqListingST25.TXT
Output Set: N:\CRF4\08142006\J502510B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 37,38,40,41,43,44
Seq#:42; N Pos. 37,38,40,41,43,44
Seq#:51; Xaa Pos. 2